BIOTE IOLOGY
SYSTEMS
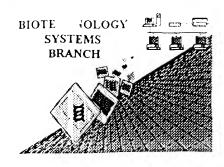BRANCH

#8

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _04/688, 286 A_

Source: _OIPE_

Date Processed by STIC: _7/5/2001_

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THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/688, 284 A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics / Wrapped Aminos — The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 _____ Invalid Line Length — The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

3 _____ Misaligned Amino Numbering — The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.

4 _____ Non-ASCII — The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**

5 _____ Variable Length — Sequence(s)_____contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 _____ PatentIn 2.0 "bug" — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7 _____ Skipped Sequences (OLD RULES) — Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
　(i)　　SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

8 _____ Skipped Sequences (NEW RULES) — Sequence(s) _____ missing. If **intentional**, please insert the following lines for **each** skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 _____ Use of n's or Xaa's (NEW RULES) — Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or **Xaa** represents.

10 ✓ Invalid <213> Response — Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence

11 _____ Use of <220> — Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 _____ PatentIn 2.0 — Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file.

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: **US/09/688,286A**

DATE: 07/05/2001
TIME: 10:37:06

Input Set : **A:\SEQUENCE.asc**
Output Set: **N:\CRF3\07052001\I688286A.raw**

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  4 <110> APPLICANT: Willson, Tracy
  5        Nicola, Nicos A.
  6        Hilton, Douglas J.
  7        Metcalf, Donald
  8        Zhang, Jian G.
 10 <120> TITLE OF INVENTION: NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES
 11        ENCODING SAME
 13 <130> FILE REFERENCE: Davies Collison Cave
 15 <140> CURRENT APPLICATION NUMBER: 09/688,286A
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C--> 16 **<141> CURRENT FILING DATE: 2001-06-20**
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 18 <150> PRIOR APPLICATION NUMBER: 09/051,843
 19 <151> PRIOR FILING DATE: 1998-06-29
 21 <160> NUMBER OF SEQ ID NOS: 11
 23 <170> SOFTWARE: PatentIn Ver. 2.0
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 1383
 27 <212> TYPE: DNA
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 32 <222> LOCATION: (61)..(1338)
 34 <220> FEATURE:
 35 <221> NAME/KEY: unsure
 36 <222> LOCATION: (121)
 37 <223> OTHER INFORMATION: n=authors are unsure of exact sequence in this
 38        region
 40 <220> FEATURE:
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 43 <223> OTHER INFORMATION: n=authors are unsure of exact sequence in this
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 49 <223> OTHER INFORMATION: n=authors are unsure of exact sequence in this
 50        region
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 53 <221> NAME/KEY: unsure
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 55 <223> OTHER INFORMATION: n=authors are unsure of exact sequence in this
 56        region
 58 <220> FEATURE:
 59 <221> NAME/KEY: unsure
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[handwritten annotations: "Does Not Comply Corrected Diskette Needed (see pups)"; "see item #10 on Error Summary Sheet."]

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Output Set: **N:\CRF3\07052001\I688286A.raw**

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        75 Met Ala Arg Pro Ala Leu Leu Gly Glu Leu Leu Val Leu Leu Leu Trp
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W-->    78 acc gcc acc gtg nnn ggc caa gtt gcc gcg gcc aca gaa gtt cag cca   156
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        83 Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Ile Ile
        84          35                  40                  45
        86 tgg acg tgg agt cct cct gaa gga gcc agt cca aat tgc act ctc aga   252
        87 Trp Thr Trp Ser Pro Pro Glu Gly Ala Ser Pro Asn Cys Thr Leu Arg
        88      50                  55                  60
        90 tat ttt agt cac ttt gat gac caa cag gat aag aaa att gct cca gaa   300
        91 Tyr Phe Ser His Phe Asp Asp Gln Gln Asp Lys Lys Ile Ala Pro Glu
        92 65                  70                  75                  80
        94 act cat cgt aaa gag gaa tta ccc ctg gat gag aaa atc tgt ctg cag   348
        95 Thr His Arg Lys Glu Glu Leu Pro Leu Asp Glu Lys Ile Cys Leu Gln
        96                  85                  90                  95
        98 gtg ggc tct cag tgt agt gcc aat gaa agt gag aag cct agc cct ttg   396
        99 Val Gly Ser Gln Cys Ser Ala Asn Glu Ser Glu Lys Pro Ser Pro Leu
       100              100                 105                 110
       102 gtg aaa aag tgc atc tca ccc cct gaa ggt gat cct gag tcc gct gtg   444
       103 Val Lys Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val
       104          115                 120                 125
       106 act gag ctc aag tgc att tgg cat aac ctg agc tat atg aag tgt tcc   492
       107 Thr Glu Leu Lys Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser
       108      130                 135                 140
       110 tgg ctc cct gga agg aat aca agc cct gac aca cac tat act ctg tac   540
       111 Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr His Tyr Thr Leu Tyr
       112 145                 150                 155                 160
       114 tat tgg tac agc agc ctg gag aaa agt cgt caa tgt gaa aac atc tat   588
       115 Tyr Trp Tyr Ser Ser Leu Glu Lys Ser Arg Gln Cys Glu Asn Ile Tyr
       116                 165                 170                 175
       118 aga gaa ggt caa cac att gct tgt tcc ttt aaa ttg act aaa gtg gaa   636
       119 Arg Glu Gly Gln His Ile Ala Cys Ser Phe Lys Leu Thr Lys Val Glu
       120              180                 185                 190
W-->   122 cct nnn agt ttt gaa cat cag aac gtt caa ata atg gtc aag gat aat   684
W-->   123 Pro Xaa Ser Phe Glu His Gln Asn Val Gln Ile Met Val Lys Asp Asn
       124          195                 200                 205
       126 gct ggg aaa att agg cca tcc tgc aaa ata gtg tct tta act tcc tat   732
       127 Ala Gly Lys Ile Arg Pro Ser Cys Lys Ile Val Ser Leu Thr Ser Tyr
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RAW SEQUENCE LISTING   DATE: 07/05/2001
PATENT APPLICATION: US/09/688,286A   TIME: 10:37:06

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Output Set: **N:\CRF3\07052001\I688286A.raw**

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135 Ala Leu Leu Val Gln Trp Lys Asn Pro Gln Asn Phe Arg Ser Arg Cys
136             245             250             255
138 tta act tat gaa gtg gag gtc aat aat act caa acc gac cga cat aat   876
139 Leu Thr Tyr Glu Val Glu Val Asn Asn Thr Gln Thr Asp Arg His Asn
140             260             265             270
142 att tta gag gtt gaa gag gac aaa tgc cag aat tcc gaa tct gat aga   924
143 Ile Leu Glu Val Glu Glu Asp Lys Cys Gln Asn Ser Glu Ser Asp Arg
144         275             280             285
146 aac atg gag ggt aca agt tgt ttc caa ctc cct ggt gtt ctt gcc gac   972
147 Asn Met Glu Gly Thr Ser Cys Phe Gln Leu Pro Gly Val Leu Ala Asp
148     290             295             300
150 gct gtc tac aca gtc aga gta aga gtc aaa aca aac aag tta tgc ttt   1020
151 Ala Val Tyr Thr Val Arg Val Arg Val Lys Thr Asn Lys Leu Cys Phe
152 305                 310             315                 320
154 gat gac aac aaa ctg tgg agt gat tgg agt gaa gca cag agt ata ggt   1068
155 Asp Asp Asn Lys Leu Trp Ser Asp Trp Ser Glu Ala Gln Ser Ile Gly
156             325             330             335
158 aag gag caa aac tcc acc ttc tac acc acc atg tta ctc acc att cca   1116
159 Lys Glu Gln Asn Ser Thr Phe Tyr Thr Thr Met Leu Leu Thr Ile Pro
160             340             345             350
162 gtc ttt gtc gca gtg gca gtc ata atc ctc ctt ttt tac ctg aaa agg   1164
163 Val Phe Val Ala Val Ala Val Ile Ile Leu Leu Phe Tyr Leu Lys Arg
164         355             360             365
166 ctt aag atc att ata ttt cct cca att cct gat cct ggc aag att ttt   1212
167 Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe
168     370             375             380
170 aaa gaa atg ttt gga gac cag aat gat gat acc ctg cac tgg aag aag   1260
171 Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys
172 385                 390             395                 400
174 tat gac atc tat gag aaa caa tcc aaa gaa gaa acg gat tct gta gtg   1308
175 Tyr Asp Ile Tyr Glu Lys Gln Ser Lys Glu Glu Thr Asp Ser Val Val
176             405             410             415
178 ctg ata gaa aac ctg aag aaa gca gct cct tgatggggag aagtgatttc     1358
179 Leu Ile Glu Asn Leu Lys Lys Ala Ala Pro
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191 <220> FEATURE:
192 <221> NAME/KEY: unsure
193 <222> LOCATION: (21)
194 <223> OTHER INFORMATION: authors are unsure about the sequence assignment
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see page 1

RAW SEQUENCE LISTING   DATE: 07/05/2001
PATENT APPLICATION: US/09/688,286A   TIME: 10:37:06

Input Set : A:\SEQUENCE.asc
Output Set: N:\CRF3\07052001\I688286A.raw

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206               20                  25                  30
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209           35                  40                  45
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212       50                  55                  60
214 Tyr Phe Ser His Phe Asp Asp Gln Gln Asp Lys Lys Ile Ala Pro Glu
215  65                  70                  75                  80
217 Thr His Arg Lys Glu Glu Leu Pro Leu Asp Glu Lys Ile Cys Leu Gln
218               85                  90                  95
220 Val Gly Ser Gln Cys Ser Ala Asn Glu Ser Glu Lys Pro Ser Pro Leu
221               100                 105                 110
223 Val Lys Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val
224               115                 120                 125
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227       130                 135                 140
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230 145                 150                 155                 160
232 Tyr Trp Tyr Ser Ser Leu Glu Lys Ser Arg Gln Cys Glu Asn Ile Tyr
233               165                 170                 175
235 Arg Glu Gly Gln His Ile Ala Cys Ser Phe Lys Leu Thr Lys Val Glu
236               180                 185                 190
W--> 238 Pro Xaa Ser Phe Glu His Gln Asn Val Gln Ile Met Val Lys Asp Asn
239               195                 200                 205
241 Ala Gly Lys Ile Arg Pro Ser Cys Lys Ile Val Ser Leu Thr Ser Tyr
242       210                 215                 220
244 Val Lys Pro Asp Pro Pro His Ile Lys His Leu Leu Leu Lys Asn Gly
245 225                 230                 235                 240
247 Ala Leu Leu Val Gln Trp Lys Asn Pro Gln Asn Phe Arg Ser Arg Cys
248               245                 250                 255
250 Leu Thr Tyr Glu Val Glu Val Asn Asn Thr Gln Thr Asp Arg His Asn
251               260                 265                 270
253 Ile Leu Glu Val Glu Glu Asp Lys Cys Gln Asn Ser Glu Ser Asp Arg
254               275                 280                 285
256 Asn Met Glu Gly Thr Ser Cys Phe Gln Leu Pro Gly Val Leu Ala Asp
257       290                 295                 300
259 Ala Val Tyr Thr Val Arg Val Arg Val Lys Thr Asn Lys Leu Cys Phe
260 305                 310                 315                 320
262 Asp Asp Asn Lys Leu Trp Ser Asp Trp Ser Glu Ala Gln Ser Ile Gly
263               325                 330                 335
265 Lys Glu Gln Asn Ser Thr Phe Tyr Thr Thr Met Leu Leu Thr Ile Pro
266               340                 345                 350
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293 <400> SEQUENCE: 3
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298 Met Glu Trp Pro Ala Arg Leu Cys Gly Leu Trp Ala Leu Leu Leu Cys
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315  65                 70                  75                  80
317 act cgt cgt tca ata gaa gta ccc ctg aat gag agg att tgt ctg caa 348
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319                 85                  90                  95
321 gtg ggg tcc cag tgt agc acc aat gag agt gag aag cct agc att ttg 396
322 Val Gly Ser Gln Cys Ser Thr Asn Glu Ser Glu Lys Pro Ser Ile Leu
323             100                 105                 110
325 gtt gaa aaa tgc atc tca ccc cca gaa ggt gat cct gag tct gct gtg 444
326 Val Glu Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val
327         115                 120                 125
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330 Thr Glu Leu Gln Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser
331     130                 135                 140
333 tgg ctc cct gga agg aat acc agt ccc gac act aac tat act ctc tac 540
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335 145                 150                 155                 160
347 tgt ...                                                       588
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VERIFICATION SUMMARY DATE: 07/05/2001
PATENT APPLICATION: **US/09/688,286A** TIME: 10:37:07

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Output Set: **N:\CRF3\07052001\I688286A.raw**

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L:79 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:122 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:123 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:205 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:238 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:551 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:571 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:589 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
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